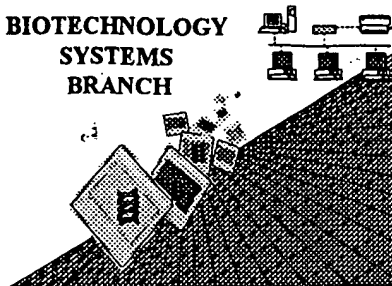




RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



TECH CENTER 1600/2900

NOV 13 2001

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COPY OF PAPERS
ORIGINALLY FILED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/554,945

Source: O/PF

Date Processed by STIC: 9/6/2001

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JUN 11 2002

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



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ORIGINALLY FILED

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/554,945

DATE: 09/06/2001
TIME: 15:07:52

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\09062001\I554945.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: CHEN, JIA-LUN
5 FU, GANG
6 SONG, HUAI-DONG
8 <120> TITLE OF INVENTION: A HUMAN HSG III GENE
11 <130> FILE REFERENCE: CPA-100US
13 <140> CURRENT APPLICATION NUMBER: 09/554,945
14 <141> CURRENT FILING DATE: 2001-08-20
16 <150> PRIOR APPLICATION NUMBER: PCT/CN98/00199
17 <151> PRIOR FILING DATE: 1998-09-22
19 <160> NUMBER OF SEQ ID NOS: 2
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2017
25 <212> TYPE: DNA
26 <213> ORGANISM: HOMO SAPIENS
W--> 27 <220> FEATURE: FEATURE
W--> 27 ~~<220> FEATURE: FEATURE~~ *delete - do not insert an alphabetical heading*
28 <221> NAME/KEY: UNSURE *when using new*
29 <222> LOCATION: (1930)(1990)(2005) *sequence header*
30 <223> OTHER INFORMATION: ~~OTHER INFORMATION~~ cDNA Sequence *format.*
32 <400> SEQUENCE: 1 *delete*

33	taaagctacg ccctggccgc agtctccgcg tcacaggaac ttcagcacc	60
34	cagegtcccc ctctacctgg agacttgact ccgcgcgcgc ccaaccctgc	120
35	accgtcgagt gtcagagatc ctgcagccgc ccagtcgccg cccctctccc	180
36	caccctcctg gctcttcttg tttttactcc tccttttcat tcataacaaa	240
37	ccaggagccc agcgcggggc tgtgacccaa gccgagcgtg gaagaatggg	300
38	accggcactt ggattctggt gttagtgtct ccgattcaag ctttcccca	360
39	agccaagaca aatctctaca taatagagaa ttaagtgcag aaagaccttt	420
40	attgctgaag cagaagaaga caagattaaa aaaacatata ctccagaaaa	480
41	caagacaact attcttttgg tgataacttg aacctgtcaa gggcaataac	540
42	aaaattgaga aagaaagaca atctataaga agctcccccac ttgataataa	600
43	gaagatgttg attcaaccaa gaatcgaaaa ctgatcgatg attatgactc	660
44	ggattggatc ataaatttca agatgatcca gatggtcttc atcaactaga	720
45	ttaaccgctg aagacattgt ccataaaaatc gctgccagga tttatgaaga	780
46	gccgtgtttg acaagattgt ttctaaacta cttaatctcg gccttatcac	840
47	gcacatacac tgggaagatga agtagcagag gttttacaaa aattaatctc	900
48	aacaattatg aggaggatcc caataagccc acaagctgga ctgagaatca	960
49	ataccagaga aagtgactcc aatggcagca attcaagatg gtcttgctaa	1020
50	gatgaaacag tatctaacac attaaccttg acaaattggt tggaaaggag	1080
51	tacagtgaag acaactttag ggacttccaa tatttcccaa atttctatgc	1140
52	agtattgatt cagaaaaaga agcaaaagag aaagaaacac tgattactat	1200
53	ctgattgact ttgtgaagat gatggtgaaa tatggaacaa tatctccaga	1260
54	tcctaccttg aaaacttgga tgaaatgatt gctcttcaga caaaaacaa	1320
55	aatgctactg acaatataag caagcttttc ccagcaccat cagagaagag	1380
56	acagacagta ccaaggaaga agcagctaag atggaaaagg aatatggaag	1440
57	tccacaaaag atgataactc caaccagga ggaaagacag atgaacccaa	1500
58	gaagcctatt tggaagccat cagaaaaaat attgaatggt tgaagaaaca	1560

never has a response; it is a "leader" only.
The CRF program inserts alphabetical headings for clarity.

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59 ggaaataaag aagattatga cctttcaaag atgagagact tcatcaataa acaagctgat 1620
 60 gcttatgtgg agaaaggcat ccttgacaag gaagaagccg aggccatcaa gcgcatttat 1680
 61 agcagcctgt aaaaatggca aaagatccag gagtctttca actgtttcag aaaacataat 1740
 62 atagcttaaa acacttctaa ttctgtgatt aaaatttttt gacccaaggg ttattagaaa 1800
 63 gtgctgaatt tacagtagtt aaccttttac aagtgggttaa aacatagctt tcttcccgtta 1860
 64 aaaactatct gaaagtaaag ttgtatgtaa gctgagattt tgtatacagg aatccttatt 1920
 65 tcttcatagn cttattatatt tataatcagg aatatgttgc tttggaaaaa gcctcttaat 1980
 66 gggctgaccc taaaaaactca atccntcttc cactgtc 2017
 68 <210> SEQ ID NO: 2
 69 <211> LENGTH: 468
 70 <212> TYPE: PRT
 71 <213> ORGANISM: HOMO SAPIENS
 73 <400> SEQUENCE: 2
 74 Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu Pro
 75 1 5 10 15
 76 Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser Leu His
 77 20 25 30
 78 Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile Ala Glu
 79 35 40 45
 80 Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro Glu Asn Lys Pro
 81 50 55 60
 82 Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu Asn Leu Leu Arg Ala
 83 65 70 75 80
 84 Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu Arg Gln Ser Ile Arg Ser
 85 85 90 95
 86 Ser Pro Leu Asp Asn Lys Leu Asn Val Glu Asp Val Asp Ser Thr Lys
 87 100 105 110
 88 Asn Arg Lys Leu Ile Asp Asp Tyr Asp Ser Thr Lys Ser Gly Leu Asp
 89 115 120 125
 90 His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp Gly Thr
 91 130 135 140
 92 Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Ala Arg Ile Tyr
 93 145 150 155 160
 94 Glu Glu Asn Asp Arg Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu
 95 165 170 175
 96 Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu
 97 180 185 190
 98 Val Ala Glu Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr
 99 195 200 205
 100 Glu Glu Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly
 101 210 215 220
 102 Lys Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
 103 225 230 235 240
 104 Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu Thr
 105 245 250 255
 106 Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn Phe Arg
 107 260 265 270
 108 Asp Phe Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys Ser Ile Asp
 109 275 280 285

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```

110 Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile Met Lys
111      290                      295                      300
112 Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr Ile Ser
113 305                      310                      315                      320
114 Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Met Ile Ala
115                      325                      330                      335
116 Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Ala Thr Asp Asn Ile Ser
117                      340                      345                      350
118 Lys Leu Phe Pro Ala Pro Ser Glu Lys Ser His Glu Glu Thr Asp Ser
119                      355                      360                      365
120 Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser Leu Lys
121      370                      375                      380
122 Asp Ser Thr Lys Asp Asp Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu
123 385                      390                      395                      400
124 Pro Lys Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile
125                      405                      410                      415
126 Glu Trp Leu Lys Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp
127                      420                      425                      430
128 Leu Ser Lys Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val
129                      435                      440                      445
130 Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile
131      450                      455                      460
132 Tyr Ser Ser Leu
133 465

```

VERIFICATION SUMMARY

DATE: 09/06/2001

PATENT APPLICATION: US/09/554,945

TIME: 15:07:53

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09062001\I554945.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:283 W: Missing Blank Line separator, <220> field identifier
L:27 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:65 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1